

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: MAERTENS, GEERT; STUYVER, LIEVEN;
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
- (ii) TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
ISOLATES
- (iii) NUMBER OF SEQUENCES: 97
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BIERMAN & MUSERLIAN
(B) STREET: 600 THIRD AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10016
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/256,568
(B) FILING DATE: 18-JUL-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP93/03325
(B) FILING DATE: 26-NOV-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP/93/402,129.6
(B) FILING DATE: 31-AUG-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP/92/403,222.0
(B) FILING DATE: 27-NOV-1992
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: CHARLES A. MUSERLIAN
(B) REGISTRATION NUMBER: 19,683
(C) REFERENCE/DOCKET NUMBER: 410.004
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 661-8000
(B) TELEFAX: (212) 661-8002

0999301.00601

(2) INFORMATION FOR SEQ ID NO: 1:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)

(viii) POSITION IN GENOME:
 (A) CHROMOSOME/SEGMENT: HCV
 (B) MAP POSITION: Position -299 of 5' end

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..27
 (D) OTHER INFORMATION: /standard_name=
 "Universal HCV primer HcPr98"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
```

CCCTGTGAGG AACTWCTGTC TTCACGC

27

## (2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:  
 (C) INDIVIDUAL ISOLATE: HCV (Okamoto et al., 1991)

(A) CHROMOSOME/SEGMENT: HCV

(ix) FEATURE:

(B) LOCATION: 1..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

21

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV

(A) CHROMOSOME/SEGMENT: HCV

(B) MAP POSITION: Position -264 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /standard\_name=  
"Universal HCV primer HcPr95"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

26

(2) INFORMATION FOR SEO ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV

(B) MAP POSITION: Position -29 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /standard\_name=  
"Universal HCV primer HcPr96"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CACTCGCAAG CACCCTATCA GGCAGT

26

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 1 (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 1

(B) MAP POSITION: position -170 of the 5' end

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard\_name= "HCV type 1 specific Probe HcPr124"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTGCCAGG ACGACC

16

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL ISOLATE: HCV type 1 (Kato et al., 1990)
- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME/SEGMENT: HCV type 1
  - (B) MAP POSITION: position -117 of 5'end
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..16
  - (D) OTHER INFORMATION: /standard\_name= "HCV type 1 specific Probe HcPr125"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCTCCAGGCA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL ISOLATE: HCV type 1b (Kato et al., 1990)
- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME/SEGMENT: HCV type 1b
  - (B) MAP POSITION: position -103 of the 5'end
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..16
  - (D) OTHER INFORMATION: /standard\_name= "HCV type 1b specific Probe HcPr138"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCGCGAGACT GCTAGC

16

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL ISOLATE: HCV type 2
- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME/SEGMENT: HCV type 2
  - (B) MAP POSITION: position -83 of the 5'end
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..16
  - (D) OTHER INFORMATION: /standard\_name= "HCV type 2 specific Probe HcPr147"

T090/0"20E66860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TAGCGTTGGG TTGCGA

16

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 2a (Chan et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 2a
- (B) MAP POSITION: position -168 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard\_name= "HCV type 2a specific probe HcPr136"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTRCCGGRAA GACTGG

16

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

0999300-00001

(viii) POSITION IN GENOME:

(B) MAP POSITION: Position -117 of 5' end

(A) NAME/KEY: misc feature

(D) OTHER INFORMATION: /standard\_name= "HCV type 2a specific probe HcPr137"

TGRC CGGGCA TAGAGT

(2) INFORMATION FOR SEQ ID NO: 11:

(A) LENGTH: 16 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2b (Nakao et al., 1991)

(A) CHROMOSOME/SEGMENT: HCV type 2b

(B) MAP POSITION: position -168 of 5' end

(A) NAME/KEY: misc\_feature

(D) OTHER INFORMATION: /standard\_name= "HCV type 2b specific probe HcPr126"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TTACCGGGAA GACTGG

16



(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL ISOLATE: HCV type 2b (Nakao et al., 1991)
- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME/SEGMENT: HCV type 2b
  - (B) MAP POSITION: position -117 of 5' end
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..16
  - (D) OTHER INFORMATION: /standard\_name= "HCV type 2b specific probe HcPr127"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGACCGGACA TAGAGT

16

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL ISOLATE: HCV type 3
- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME/SEGMENT: HCV type 3
  - (B) MAP POSITION: position -170 of 5' end

(D) OTHER INFORMATION: /standard\_name= "HCV type  
3 specific probe HcPr128"

16

(D) TOPOLOGY: linear

(D) OTHER INFORMATION: /standard\_name= "HCV type  
3 specific probe HcPr 129"

16

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(C) INDIVIDUAL ISOLATE: HCV type 3a (Chan et al., 1992)

(A) CHROMOSOME/SEGMENT: HCV type 3a

(B) MAP POSITION: position -146 of 5' end

(A) NAME/KEY: misc feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard\_name= "HCV type 3a specific probe HcPr140"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCTTGGAGCA ACCCGC

16

(2) INFORMATION FOR SEQ ID NO: 16:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(C) INDIVIDUAL ISOLATE: HCV type 3b (Chan et al., 1992)

(A) CHROMOSOME/SEGMENT: HCV type 3b

(B) MAP POSITION: position -146 of 5' end

(A) NAME/KEY: misc feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard\_name= "HCV type 3b specific probe HcPr139"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TCTTGGGAACA ACCCGC

16

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 4 (Bukh et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 4
- (B) MAP POSITION: position -170 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard\_name= "HCV type 4 specific probe HcPr 144"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AATYGCCGGG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

099070"20666660

- (vi) ORIGINAL SOURCE:  
    (C) INDIVIDUAL ISOLATE: HCV type 4
- (viii) POSITION IN GENOME:  
    (A) CHROMOSOME/SEGMENT: HCV type 4  
    (B) MAP POSITION: position -147 of 5' end
- (ix) FEATURE:  
    (A) NAME/KEY: misc\_feature  
    (B) LOCATION: 1..16  
    (D) OTHER INFORMATION: /standard\_name= "HCV type  
        4 specific probe HcPr145"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTCTTGGAAC TAACCC

16

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:  
    (C) INDIVIDUAL ISOLATE: HCV type 4
- (viii) POSITION IN GENOME:  
    (A) CHROMOSOME/SEGMENT: HCV type 4  
    (B) MAP POSITION: position -117 of 5' end
- (ix) FEATURE:  
    (A) NAME/KEY: misc\_feature  
    (B) LOCATION: 1..16  
    (D) OTHER INFORMATION: /standard\_name= "HCV type  
        4 specific probe HcPr146"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTCCGGGCA TTGAGC

16

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- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..16  
 (D) OTHER INFORMATION: /standard\_name= "HCV type  
 3 specific probe HcPr 154"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CCGCGAGATC ACTAGC

16

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:  
 (C) INDIVIDUAL ISOLATE: HCV type 2a (Okamoto et  
 al., 1991)

- (viii) POSITION IN GENOME:  
 (A) CHROMOSOME/SEGMENT: HCV type 2a  
 (B) MAP POSITION: position -165 of 5' end

- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..16  
 (D) OTHER INFORMATION: /standard\_name= "HCV type  
 2a specific probe HcPr156"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CCGGGAAGAC TGGGTC

16

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

09899303.070001

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: HCV type 2b (Okamoto et al., 1992)
- (viii) POSITION IN GENOME:  
(A) CHROMOSOME/SEGMENT: HCV type 2b  
(B) MAP POSITION: position - 165 of 5' end
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..16  
(D) OTHER INFORMATION: /standard\_name= "HCV type 2b specific probe HcPr157"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CCGGAAAGAC TGGGTC

16

- (2) INFORMATION FOR SEQ ID NO: 24:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: HCV type 2a (Okamoto et al., 1991)
- (viii) POSITION IN GENOME:  
(A) CHROMOSOME/SEGMENT: HCV type 2a  
(B) MAP POSITION: position -136 of 5' end
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..16  
(D) OTHER INFORMATION: /standard\_name= "HCV type 2a specific probe HcPr158"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ACCCACTCTA TGCCCCG

16

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 2b (Okamoto et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 2b
- (B) MAP POSITION: position -136 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard\_name= "HCV type 2b specific probe HcPr159"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCCACTCTA TGTCCG

16

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

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(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2 (Okamoto et al., 1992)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 2

(B) MAP POSITION: position -126 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard\_name= "HCV type 2 specific probe HcPr160"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATAGAGTGGG TTTATC

16

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV

(B) MAP POSITION: Position -195 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard\_name= "Universal HCV probe HcPr153"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TCTGCGGAAC CGGTGA

16

0999'0" 20E66666

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

AATTGCCAGG AYGACC

16

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GCTCAGTGCC TGGAGA

16

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

09899300-070601

CCGCGAGACY GCTAGC

16

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

CCCCGCAAGA CTGCTA

16

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

CGTACAGCCT CCAGGC

16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGACCCAGTC TTCCTG

16

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TGCCTGGTCA TTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TKTCTGGGTA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

16

16

16

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GAGTGTGTGTG CAGCCT

16

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

AATCGCCGGG ACGACC

16

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

0989800-0501

AATGCCCGGC AATTG

16

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AATCGCCGAG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AATGCTCGGA AATTG

16

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA



(iii) ANTI-SENSE: NO

GAGTGTCGAA CAGCCT

16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

AATTGCCGGG ATGACC

16

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TCTCCGGGCA TTGAGC

16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

16

(D) TOPOLOGY: linear

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

16

(D) TOPOLOGY: linear

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

16



AGTYCACCGG AATCGC

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

16

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

16

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: jp62

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

|                                             |     |
|---------------------------------------------|-----|
| GAGTGTCGTA CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC | 80  |
| CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG | 120 |
| CCCGGCCATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA | 160 |
| GTAGCGTTGG GTTGCGA                          | 177 |

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb81

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

|                                             |     |
|---------------------------------------------|-----|
| GAGTGTCGTA CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC | 80  |
| CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG | 120 |
| CCCGGTCATT TGGGCGTGCC CCCGCAAGAC CGCTAGCCGA | 160 |
| GTAGCGTTGG GTTGCGA                          | 177 |

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid

0989302.00001

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: br56

(viii) POSITION IN GENOME:  
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

|                                              |     |
|----------------------------------------------|-----|
| GAGTGTCTGTG CAGCCTCCAG GGGGGGGGGT CCCGGGAGAG | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC  | 80  |
| TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA  | 120 |
| CCCAGAAATT TGGGCGTGCC CCCGCGAGAT CACTAGCCGA  | 160 |
| GTAGTGTTGG GTCGCGA                           | 177 |

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: bu79

(viii) POSITION IN GENOME:  
(B) MAP POSITION: 5'untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

|                                              |     |
|----------------------------------------------|-----|
| GAGTGTTGTA CAGCCTCCAG GGGGGGGGGT CCCGGGAGAG  | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC  | 80  |
| CGGGACGACC GGGTCCTTTC TTGGATTAAAC CCGCTCAATG | 120 |
| CCCGGAAATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA  | 160 |
| GTAGTGTTGG GTCGCGA                           | 177 |

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 178 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: bu74

- (viii) POSITION IN GENOME:
  - (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

|                                              |     |
|----------------------------------------------|-----|
| GAGTGTGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG    | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTCCA CCGGAATCGC  | 80  |
| CGGGATGACC GGGTCCTTTC TTGGAATAA CCCGCTCAAT   | 120 |
| GCCCGGAAAT TTGGGCGTGC CCCC GCGAGA CTGCTAGCCG | 160 |
| AGTAGTGTG GGTGCGCA                           | 178 |

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 178 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: gb80

- (viii) POSITION IN GENOME:
  - (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

|                                             |     |
|---------------------------------------------|-----|
| GAGTGTCGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG  | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC | 80  |
| CGGGATGACC GGGTCCTTTC TTGGAATAA CCCGCTCAAT  | 120 |

GCGCCGAAAT TTGGGCGTGC CCCCGCGAGA CTGCTAGCCG 160  
 AGTAGTGTTG GGTCGCGA 178

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: be82 (also referred to as be99)

- (viii) POSITION IN GENOME:  
(B) MAP POSITION: 5' untranslated region

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

|             |            |            |            |     |
|-------------|------------|------------|------------|-----|
| GAGTGTCTGTG | CAGCCTCCAG | GACCCCCCT  | CCCGGGAGAG | 40  |
| CCATAGTGGT  | CTGCGGAACC | GGTGAGTACA | CCGGAATTGC | 80  |
| CAGGACGACC  | GGGTCCTTTC | TTGGATCAAC | CCGCTCAATG | 120 |
| CCTGGAGATT  | TGGGCGTGCC | CCCGCGAGAC | CGCTAGCCGA | 160 |
| GTAGTGTGG   | GTCGCGA    |            |            | 177 |

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: be90

- (viii) POSITION IN GENOME:  
(B) MAP POSITION: 5' untranslated region

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GAGTGTCGTG CAGCCTCCAG GATCCCCCCT CCCGGGAGAG 40



CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC 80  
CAGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAGTG 120  
CCTGGAGATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA 160  
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be91

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GAGTGTCGTA CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG 40  
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC 80  
CGGAAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG 120  
TCCGGTCATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCTA 160  
GTAGCGTTGG GTTGCGA 177

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be92

099999.0000

- (viii) POSITION IN GENOME:  
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

|                                              |     |
|----------------------------------------------|-----|
| GAGTGTCTGTA CAGCCTCCAG GCGGGGGGCT CCCGGGAGAG | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC  | 80  |
| CAGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG  | 120 |
| CCTGGTCATT TGGGCGTGCC CCGCAAGAC TGCTAGCCGA   | 160 |
| GTCGCTTGG GTTGCGA                            | 177 |

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: be93

(viii) POSITION IN GENOME:  
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

|                                              |     |
|----------------------------------------------|-----|
| GAGTGTCTGTG CAGCCTCCAG GCGGGGGGCT CCCGGGAGAG | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC  | 80  |
| TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA  | 120 |
| CCCAGACATT TGGGCGTGCC CCGCGAGAT CACTAGCCGA   | 160 |
| GTCGCTTGG GTCGCGA                            | 177 |

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

0959302-07004  
105070-2055550

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: be94

(viii) POSITION IN GENOME:  
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

|                                             |     |
|---------------------------------------------|-----|
| GAGTGTCTGTG CAGCCTCCAG GGGGGGGCT CCCGGGAGAG | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC | 80  |
| TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA | 120 |
| CCCAGACATT TGGGCGTGCC CCCGCAAGAT CACTAGCCGA | 160 |
| GTAGTGTGG GTCGCGA                           | 177 |

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: gb48

(viii) POSITION IN GENOME:  
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

|                                             |     |
|---------------------------------------------|-----|
| GAGTGTTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG  | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC | 80  |
| CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG | 120 |
| CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA | 160 |
| GTAGTGTGG GTCGCGA                           | 177 |

0999306.00001

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb116

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

|                                              |     |
|----------------------------------------------|-----|
| GAGTGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC  | 80  |
| CGGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG  | 120 |
| CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA  | 160 |
| GTAGTGTGTTGG GTCGCGA                         | 177 |

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb569

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

|                                              |     |
|----------------------------------------------|-----|
| GAGTGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC  | 80  |
| CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG  | 120 |

0999303-070601

CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA 160  
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb358

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GAGTGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG 40  
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC 80  
CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG 120  
CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA 160  
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb549

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

0999302-07001

|            |            |            |            |     |
|------------|------------|------------|------------|-----|
| GAGTGTGTG  | CAGCCTCCAG | GACCCCCCT  | CCCGGGAGAG | 40  |
| CCATAGTGGT | CTGCGGAACC | GGTGAGTTCA | CCGGAATCGC | 80  |
| CGGGACGACC | GGGTCTTTT  | TTGGAACAAA | CCCGCTCAAT | 120 |
| GCCCGGCAAT | TTGGGCGTGC | CCCCGCAAGA | CTGCTAGCCG | 160 |
| AGTAGTGTTG | GGTCGCGA   |            |            | 178 |

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: cam600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

|            |            |            |            |     |
|------------|------------|------------|------------|-----|
| GAGTGTGTA  | CAGCCTCCAG | GACCCCCCT  | CCCGGGAGAG | 40  |
| CCATAGTGGT | CTGCGGAACC | GGTGAGTACA | CCGGAATCGC | 80  |
| CGAGATGACC | GGGTCCTTTC | TTGGATCAAC | CCGCTCAATG | 120 |
| CTCGGAAATT | TGGGCGTGCC | CCCGCAAGAC | TGCTAGCCGA | 160 |
| GTAGTGTGG  | GTCGCGA    |            |            | 177 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(B) CLONE: cam736

(B) MAP POSITION: 5' untranslated region

|            |            |            |            |     |
|------------|------------|------------|------------|-----|
| GAGTGTGTA  | CAGCCTCCAG | GACCCCCCT  | CCCGGGAGAG | 40  |
| CCATAGTGGT | CTGCGGAACC | GGTGAGTACA | CCGGAATCGC | 80  |
| CGAGATGACC | GGGTCCTTTC | TTGGATCAAC | CCGCTCAATG | 120 |
| CTCGGAAATT | TGGGCGTGCC | CCCGCAAGAC | TGCTAGCCGA | 160 |
| GTAGTGTG   | GTCGCGA    |            |            | 177 |

(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(B) CLONE: qb809

(B) MAP POSITION: 5' untranslated region

|             |            |            |            |     |
|-------------|------------|------------|------------|-----|
| GAGTGTGTGTA | CAGCCTCCAG | GACCCCCCT  | CCCGGGAGAG | 40  |
| CCATAGTGGT  | CTGCGGAACC | GGTGAGTACA | CCGGAATCGC | 80  |
| CGAGATGACC  | GGGTCCTTTC | TTGGATCAAC | CCGCTCAATG | 120 |
| CTCGGAAATT  | TGGGCGTGCC | CCCGCAAGAC | CGCTAGCCGA | 160 |
| GTAGTGTGG   | GTCGCGA    |            |            | 177 |

(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb487

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

|                                             |     |
|---------------------------------------------|-----|
| GAGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG   | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC | 80  |
| CAGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG | 120 |
| CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA | 160 |
| GTAGTGTGTTGG GTCGCGA                        | 177 |

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb724

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

|                                             |     |
|---------------------------------------------|-----|
| GAGTGTCGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG  | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTTCA CCGGAATCGC | 80  |
| CAGGACGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG | 120 |
| CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA | 160 |
| GTAGTGTGTTGG GTCGCGA                        | 177 |



(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 177 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
    (A) LIBRARY: be97

(viii) POSITION IN GENOME:  
    (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

|                                             |     |
|---------------------------------------------|-----|
| GAGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG   | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC | 80  |
| CAGGACGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG | 120 |
| CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA | 160 |
| GTAGTGTGG GTCGCGA                           | 177 |

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 177 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
    (B) CLONE: be95

(viii) POSITION IN GENOME:  
    (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

|                                             |     |
|---------------------------------------------|-----|
| GAGTGTCGAA CAGCCTCCAG GACCCCCCT CCCGGGAGAG  | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC | 80  |
| CGGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG | 120 |

109920-205555

CCCGGAGATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA 160  
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: be96
- (viii) POSITION IN GENOME:
  - (B) MAP POSITION: 5' untranslated region
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

GAGTGTCGAA CAGCCTCCAG GACCCCCCT CCCGGGAGAG 40  
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC 80  
CGGGACGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG 120  
CCCGGAGATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA 160  
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: be98
- (viii) POSITION IN GENOME:
  - (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

|                                              |     |
|----------------------------------------------|-----|
| GAGTGTCTGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG  | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC  | 80  |
| CGGGTTGACC GGGTCCTTTC TTGGAAC TAC CCGCTCAATG | 120 |
| CCCGGAAATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA  | 160 |
| GTAGTGTTGG GTCGCGA                           | 177 |

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb438

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

|                                              |     |
|----------------------------------------------|-----|
| GAGTGTCTGAA CAGCCTCCAG GATCCCCCT CCCGGGAGAG  | 40  |
| CCATAGTGGT CTGCGGAACC GGTGAGTTCA CCGGAATCGC  | 80  |
| CGGGATGACC GGGTCCTTTC TTGGAATCAA CCCGCTCAAT  | 120 |
| GCCCGGAAAT TTGGGCGTGC CCCC GCGAGA CTGCTAGCCG | 160 |
| AGTAGTGTTG GGTCGCGA                          | 178 |

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1099070-2055550

(vii) IMMEDIATE SOURCE:

(B) CLONE: be90

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu
1 5 10
Ser Ile Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala
15 20
Arg Gln Ala Ile Lys Ser Leu Thr Glu Arg Leu Tyr
25 30 35
Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu
50 55 60
Thr Thr Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu
65 70
Lys Ala Ser Ala Ala Cys Arg Ala Ala Lys Leu Gln
75 80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala
100 105
Ala Ser Leu Arg Val
110

```

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: be91

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu
1 5 10
Ser Ile Tyr Gln Ala Cys Ser Leu Pro Gln Glu Ala
15 20

```

0999002-070001

(2) INFORMATION FOR SEQ ID NO: 84:

(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Val | Thr | Glu | Arg | Asp | Ile | Arg | Thr | Glu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |
| Ser | Ile | Tyr | Leu | Ala | Cys | Ser | Leu | Pro | Glu | Gln | Ala |
|     |     | 15  |     |     |     |     | 20  |     |     |     |     |
| Arg | Thr | Ala | Ile | His | Ser | Leu | Thr | Glu | Arg | Leu | Tyr |
| 25  |     |     |     | 30  |     |     |     |     |     | 35  |     |
| Val | Gly | Gly | Pro | Met | Leu | Asn | Ser | Lys | Gly | Gln | Thr |
|     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Gly | Tyr | Arg | Arg | Cys | Arg | Ala | Ser | Gly | Val | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Thr | Thr | Ser | Met | Gly | Asn | Thr | Ile | Thr | Cys | Tyr | Val |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |
| Lys | Ala | Gln | Ala | Ala | Cys | Lys | Ala | Ala | Gly | Ile | Ile |
|     |     | 75  |     |     |     |     | 80  |     |     |     |     |
| Ala | Pro | Thr | Met | Leu | Val | Cys | Gly | Asp | Asp | Leu | Val |
| 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |

Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu  
 100 105  
 Arg Asn Leu Arg Ala  
 110

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be93

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu  
 1 5 10  
 Glu Ile Tyr Gln Cys Cys Asn Leu Glu Pro Glu Ala  
 15 20  
 Arg Lys Val Ile Ser Ser Leu Thr Glu Arg Leu Tyr  
 25 30 35  
 Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln  
 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu  
 50 55 60  
 Pro Thr Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile  
 65 70  
 Lys Ala Thr Thr Ala Ala Lys Ala Ala Gly Leu Arg  
 75 80  
 Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg  
 100 105  
 Ala Ala Leu Arg Ala  
 110

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

099970-2056550

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb48

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
1 5 10
Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
 15 20
Arg Lys Ala Ile Thr Ala Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50 55 60
Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
 65 70
Lys Ala Ser Ala Ala Ile Lys Ala Ala Gly Leu Arg
75 80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys
 100 105
Arg Pro Leu Gly Ala
110

```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb116

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
1 5 10

```

09999302-070604

Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala  
 15 20  
 Arg Arg Ala Ile Thr Ala Leu Thr Glu Arg Leu Tyr  
 25 30 35  
 Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu  
 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr  
 50 55 60  
 Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu  
 65 70  
 Lys Ala Ser Ala Ala Ile Arg Ala Ala Gly Leu Arg  
 75 80  
 Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys  
 100 105  
 Arg Ala Leu Gly Ala  
 110

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb215

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu  
 1 5 10  
 Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala  
 15 20  
 Arg Lys Val Ile Thr Ala Leu Thr Glu Arg Leu Tyr  
 25 30 35  
 Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu  
 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr  
 50 55 60  
 Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu  
 65 70  
 Lys Ala Ser Ala Ala Ile Arg Ala Ser Gly Leu Arg  
 75 80

109920-2055550



(2) INFORMATION FOR SEQ ID NO: 89:

(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

(2) INFORMATION FOR SEQ ID NO: 90:

(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb549

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

|     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|
| Ser | Thr | Val | Thr | Glu | Arg | Asp | Ile | Arg | Thr | Glu | Glu |  |  |  |  |  |  |  |  |  |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |  |  |  |  |  |  |  |  |  |  |  |
| Glu | Ile | Tyr | Gln | Cys | Cys | Asp | Leu | Glu | Pro | Glu | Ala |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 15  |     |     |     | 20  |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |
| Arg | Lys | Val | Ile | Ser | Ala | Leu | Thr | Glu | Arg | Leu | Tyr |  |  |  |  |  |  |  |  |  |  |  |
| 25  |     |     |     | 30  |     |     |     | 35  |     |     |     |  |  |  |  |  |  |  |  |  |  |  |
| Val | Gly | Gly | Pro | Met | Tyr | Asn | Ser | Lys | Gly | Asp | Leu |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 40  |     |     | 45  |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |
| Cys | Gly | Gln | Arg | Arg | Cys | Arg | Ala | Ser | Gly | Val | Tyr |  |  |  |  |  |  |  |  |  |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |  |  |  |  |  |  |  |  |  |  |  |
| Thr | Thr | Ser | Phe | Gly | Asn | Thr | Val | Thr | Cys | Tyr | Leu |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 65  |     |     | 70  |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |
| Lys | Ala | Val | Ala | Ala | Thr | Arg | Ala | Ala | Gly | Leu | Lys |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 75  |     |     | 80  |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |
| Gly | Cys | Ser | Met | Leu | Val | Cys | Gly | Asp | Asp | Leu | Val |  |  |  |  |  |  |  |  |  |  |  |
| 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |  |  |  |  |  |  |  |  |  |
| Val | Ile | Cys | Glu | Ser | Gly | Gly | Val | Glu | Glu | Asp | Ala |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |  |  |  |  |  |  |  |  |  |  |  |
| Arg | Ala | Leu | Arg | Ala |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 110 |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: gb809

1099070-20E55550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu
1 5 10
Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
15 20
Arg Lys Val Ile Ala Ala Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50 55 60
Thr Thr Ser Phe Gly Asn Thr Met Thr Cys Tyr Leu
65 70
Lys Ala Ser Ala Ala Ile Arg Ala Ala Gly Leu Lys
75 80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys
100 105
Arg Ala Leu Gly Ala
110

```

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be95

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu
1 5 10
Ser Ile Tyr Gln Ser Cys Asp Leu Gln Pro Glu Ala
15 20
Arg Ala Ala Ile Arg Ser Leu Thr Gln Arg Leu Tyr
25 30 35
Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe
50 55 60

```

09993002-070001

Thr Thr Ser Met Gly Asn Thr Met Thr Cys Tyr Ile  
65 70  
Lys Ala Leu Ala Ser Cys Arg Ala Ala Arg Leu Arg  
75 80  
Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val  
85 90 95  
Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu  
100 105  
Ala Ser Leu Arg Ala  
110

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GAGTGTGTGTA CAGCCTCC

18

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

TGCCCGGAAA TTTGGGC

17

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

TGCCCCGGAGA TTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GAGTGTGGAA CAGCCTC

17

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GGGGGCCTGG AGGCTG

16

| Variable                     | Mean | SD   | Min | Max  |
|------------------------------|------|------|-----|------|
| Age                          | 34.5 | 10.2 | 21  | 55   |
| Gender                       | 0.5  | 0.5  | 0   | 1    |
| Marital status               | 0.6  | 0.5  | 0   | 1    |
| Education                    | 12.5 | 1.5  | 9   | 16   |
| Income                       | 1500 | 500  | 500 | 3000 |
| Health status                | 0.7  | 0.4  | 0   | 1    |
| Smoking status               | 0.3  | 0.5  | 0   | 1    |
| Alcohol consumption          | 0.2  | 0.4  | 0   | 1    |
| Exercise frequency           | 0.5  | 0.5  | 0   | 1    |
| Stress level                 | 0.6  | 0.5  | 0   | 1    |
| Sleep quality                | 0.7  | 0.4  | 0   | 1    |
| Work satisfaction            | 0.6  | 0.5  | 0   | 1    |
| Life satisfaction            | 0.7  | 0.4  | 0   | 1    |
| Overall health               | 0.8  | 0.3  | 0   | 1    |
| Physical activity            | 0.4  | 0.5  | 0   | 1    |
| Mental health                | 0.6  | 0.4  | 0   | 1    |
| Social support               | 0.5  | 0.5  | 0   | 1    |
| Work-life balance            | 0.6  | 0.4  | 0   | 1    |
| Financial stability          | 0.7  | 0.3  | 0   | 1    |
| Family harmony               | 0.8  | 0.2  | 0   | 1    |
| Personal growth              | 0.6  | 0.4  | 0   | 1    |
| Community involvement        | 0.5  | 0.5  | 0   | 1    |
| Environmental awareness      | 0.7  | 0.3  | 0   | 1    |
| Cultural appreciation        | 0.8  | 0.2  | 0   | 1    |
| Artistic expression          | 0.6  | 0.4  | 0   | 1    |
| Volunteer work               | 0.5  | 0.5  | 0   | 1    |
| Charitable contributions     | 0.4  | 0.4  | 0   | 1    |
| Philanthropic activities     | 0.3  | 0.3  | 0   | 1    |
| Leadership roles             | 0.2  | 0.2  | 0   | 1    |
| Networking efforts           | 0.1  | 0.1  | 0   | 1    |
| Professional development     | 0.6  | 0.4  | 0   | 1    |
| Continuous learning          | 0.7  | 0.3  | 0   | 1    |
| Adaptability to change       | 0.8  | 0.2  | 0   | 1    |
| Resilience to stress         | 0.9  | 0.1  | 0   | 1    |
| Emotional regulation         | 0.7  | 0.3  | 0   | 1    |
| Conflict resolution skills   | 0.6  | 0.4  | 0   | 1    |
| Decision-making abilities    | 0.8  | 0.2  | 0   | 1    |
| Time management              | 0.7  | 0.3  | 0   | 1    |
| Organization skills          | 0.6  | 0.4  | 0   | 1    |
| Communication effectiveness  | 0.8  | 0.2  | 0   | 1    |
| Team collaboration           | 0.7  | 0.3  | 0   | 1    |
| Leadership potential         | 0.6  | 0.4  | 0   | 1    |
| Innovation in work           | 0.5  | 0.5  | 0   | 1    |
| Problem-solving skills       | 0.8  | 0.2  | 0   | 1    |
| Attention to detail          | 0.7  | 0.3  | 0   | 1    |
| Time efficiency              | 0.6  | 0.4  | 0   | 1    |
| Productivity levels          | 0.8  | 0.2  | 0   | 1    |
| Workload management          | 0.7  | 0.3  | 0   | 1    |
| Stress management techniques | 0.6  | 0.4  | 0   | 1    |
| Work-life balance strategies | 0.5  | 0.5  | 0   | 1    |
| Financial planning           | 0.4  | 0.4  | 0   | 1    |
| Investment decisions         | 0.3  | 0.3  | 0   | 1    |
| Retirement planning          | 0.2  | 0.2  | 0   | 1    |
| Health insurance coverage    | 0.9  | 0.1  | 0   | 1    |
| Life insurance policies      | 0.8  | 0.2  | 0   | 1    |
| Emergency fund status        | 0.7  | 0.3  | 0   | 1    |
| Debt management              | 0.6  | 0.4  | 0   | 1    |
| Financial literacy           | 0.5  | 0.5  | 0   | 1    |
| Investment knowledge         | 0.4  | 0.4  | 0   | 1    |
| Financial goals setting      | 0.3  | 0.3  | 0   | 1    |
| Financial discipline         | 0.2  | 0.2  | 0   | 1    |
| Financial stability index    | 0.1  | 0.1  | 0   | 1    |
| Overall financial health     | 0.0  | 0.0  | 0   | 1    |